

FIGURE 1

Fucosyltransferase nucleotide sequence from strain 1182 FutB (SEQ ID NO:1)

atgtccaaccctattagacgcttatatagaaagcgcttcattgaaaaattacctctaaatctccccccccctaaaaatcgctg
tggcgaattggtggggagatgaagaggttgaagaatttaaaagaacattctttatttctcagtcagcattacacaatcacct
ccacaaaacccaacgaacctccgatctcgtcttggcagtcctattggatcagccagaaaaatcttacctatcaaacgcaa
aaagagtgtttacaccggtgaaacgaatcgctaattcaacctcttgattacgccataggcttgatgaattggatttagagat
cgttatttaagaatgcctttatattatgatagactacaccataaagccgagagcgtgaatgacaccacttcgccttacaactcaaac
ctgacagcctttatgctttaaaaaacccctcccatcttttaagaaaaccacccaatttatgcgtagtagtgaacaatgagagcg
atcctttgaaaagaggggttgcgagttttagcgagcaaccctaacgctcctaaaaggaatgcttctatgacgttttaattctata
gagccagttattgggggagggagcgtgaaaaacactttaggctataacattaaaaacaagagcgagttttaagccaatacaaat
tcaatctgtgtttgaaaactcacaaggctatggctatgtaactgaaaaaatcattgacgcttactttagccataccattcctattattg
ggggagtcctagcgtggcacaagattttaaccctaagagtttgtgaatgtttgattttaagattttgatgaagcgattgatcatgt
gcgatacttgcacacgcacccaacgcttatttagacatgctttatgaaaaccctttaaacacccttgatgggaaagcttactttac
caaatgtgagttttaaaaaatcctagattttttaaacgattttagaaaacgacacgatttatcacgataaccctttatttttatcgt
gatttgaatgagccgtaataatctattgatgatgattgagggtaattatgatgattgagggtaattatgatgattgagggtaatta
tgatgattgagggtaattatgatgattgagggtaattatgatgattgagggtaattatgatgattgagggtaattatgatgatt
gagggtaattatgatgattgagggtaattatgatgattgagggtaattatgatgattgagggtaattatgagcggctctaca
aaacgcctcgctttattagaactctctaaaacaccacttttaaatctatcgcaaagcttatcaaaaatcctacctttgttgcgtgc
ggcgagaaagttgattaaaaaattgggtttaa

Protein sequence from strain 1182 FutB (SEQ ID NO:2)

mfqplldayiesasiekitskppplkiavanwwgdeeevefkknilyfilsqhytitlhqnpnepsdlvfgspigsarkilsy
qnakrvfytgenespnfnlfdyaigfdeldfrdrylrmplydrllhkaesvndttspyklkpdslyalkkpshhfkcnhpn
cavvnnesdplkrghasfvasnpnapknafydvlnsiepvigggsvkntlgyniknkseflsqyfnlcfensqgygyvte
kiidayfshtipiywgspsvaqdfnpksfvnvcdfkdfdeaidhvrylhthpnayldmlyenplntldgkayfyqnlsfki
ldffktilendtiyhdnpfiyrdlneplisiddlrnyddlrnyddlrnyddlrnyddlrnyddlrnyddlrnyddlrnydd
lrnyddlrnyddlrnyddlrnyerllqnaspllelsqnttfkiyrkayqkspllraarklikklgl*

FIGURE 2

Fucosyltransferase from strain 1111 FutA

Nucleotide coding sequence (SEQ ID NO:3)

atgttccaaccctattagatgcctttatagaaagcgctccattgaaaaatggcctctaatactccccccctaaaaatcgctgtgg
cgaattggtggggagatgaagaaattaaaaatttaaaaagagcgttctttattttatcctaagccagcattacacaatcactttaca
ccgaaaccctgataaacctgcggacatcgtctttggtaaccccttgatcagccagaaaaatcttatcctatcaaaacgcaaaaa
gggtgttttacaccggtgaaaatgaagtcctaactcaacctcttgattacgccataggcttgatgaattggactttagagatcgt
tatttgagaatgcctttgtattatgcctatttgcaattataaagccgagcttgtaatgacaccacttcgcctataaaactccaacctgaca
gcctttatgctttaaaaaaccctcccatcattttaaagaaaaccaccccaatttggtgcgcagtagtgaataatgagagtgcctttg
aaaagagggttgcgagctttgtcgcaagcaaccctaacgctcctagaaggaacgcttttatgaggctttaaacgctattgagcc
agttgctgggggagggagcgtgaaaaacactttaggctataatgtcaaaaacaagagcgagttttaagccaatacaaatcaat
ctgtgtttgaaaacactcaaggctatggctatgtaactgaaaagatcattgacgcttatttcagccataaccattcctattattggggg
agtcccagcgtggcgaaagattttaaccctaagagttttgtgaatgtccatgatttcaacaactttgatgaagcgattgactatatca
gatactgcacacgcacccaaacgcttatttagacatgcactatgaaaaccctttaaacactattgatgggaaagcttactttacca
aaatttgagttttaaaaaatcctagattttttaaaacgattttagaaaacgacacgatctatcacgataaccctttcattttctatcgtg
atttgatgagccttcagtatctattgatggtttgagggttaattatgatgattgagggttaattatgatgatttgagggttaattatgat
gatttgagggttaattatgagcgcctttacaaaacgcctcgcctttattagaactctctcaaaacaccacttttaaatctatcgcaaa
gcttatcaaaaatccttgcccttggtgcgtgccataaggagatgggttaaaaagtaa

Protein sequence (SEQ ID NO:4)

mfqplldafiesaplkkwplnlpplkiavanwwgdeeikfkksvlyfilsqhytitlhrnpdkpadivfgnplgsarkilsy
qnakrvfytgenevpnfnlfdyaigfdeldfrdrylrmpllyaylhykaelvndttspyklqpdslalkkpshhfkcnhpn
lcavvnnesdplkrghasfvasnprnafyealnaiepvagggsvkntlgynvknkseflsqyknfclfentqgygyvt
ekiidayfshtipiywgspsvakdfnpksfvnvhdffmfdeaidyirylhthpnayldmhyenplntidgkayfyqnlsfk
kildffktilendtiyhdnpfifyrldnepsvsidglrvnyddlrnyddlrnyddlrnyerllqnaspllelsqnttfkiyrka
yqkslpllrairrvvkk*

FIGURE 3

Strain 1218 FutB nucleotide sequence (SEQ ID NO:5)

atgtccaaccctattagacgcttatatagaagcgcttcattgaaaaattacctctaatactccccccccctaaaaatcgctg
tggcgaattggtggggagatgaagagggtgaagaattaaaaagaacattctttatttctcagtcagcattacacaatcacct
ccacaaaaccccaacgaacctccgatctcgtctttggcagtcctattggatcagccagaaaaatcttacctatcaaacgcaa
aaagagtgtttacaccggtgaaaacgaatcgctaatttcaacctctttgattacgcataggctttgatgaattggatttagagat
cgtatttaagaatgcctttatattatgatagactacaccataaagccgagagcgtgaatgacaccacttcgcttacaaactcaaac
ctgacagcctttatgctttaaaaaacccctccatcattttaagaaaaccaccccaatttatgcgcagtagtgaacaatgagagcg
atcctttgaaaagagggtttgcgagttttgtagcgagcaacctaacgctcctaaaaggaatgctttctatgacgcttaaatctata
gagccagtattgggggaggagcgtgaaaaacactttaggctataacattaaaaacaagagcgagttttaagccaatacaaat
tcaatctgtgtttgaaaactcacaaggctatggctatgtaactgaaaaaatcattgacgcttactttagccataccattcctattattg
ggggagtccttagcgtggcacaagattttaaccctaagagttttgtgaatgtttgtgattttaagattttgatgaagcgattgatcatgt
gcgatacttgcacacgcacccaaacgcttatttagacatgctttatgaaaaccctttaaacacccttgatgggaaagcttacttttac
caaaatttgagttttaaaaaaatcctagattttttaaacgatcttagaaaacgacacgatttatcacgataaccctttatttttatcgt
gatttgaatgagccgttaatatctattgatgatttgagggttaattatgatgatttgagggttaattatgatgatttgagggttaattatga
tgatttgagggttaattatgatgatttgagggttaattatgatgatttgagggttaattatgatgatttgagggttaattatgatgatttg
gggttaattatgatgatttgagggttaattgtgatgatttgagggttaattatgatgatttgagggttaattatgagcggctcttacaaa
acgcctcgcctttattagaactctctcaaacaccacttttaaaatctatcgaaagcttatcaaaaatccttacctttgttgcgtgcgg
cgagaaagtgtattaaaaaattgggtttgtaa

Predicted protein strain 1218 FutB (SEQ ID NO:6)

mfqplldayiesasiekitskspplkiavanwwgdeeeefkknilyfilsqhytitlhqnpnepsdlvfgspigsarkilsy
qnakrvfytgenespnfnldyaigfdeldfrdrylrmplyydrllhhaesvndttspyklkpdslyalkkpshhfenhpn
cavvnnesdplkrghasfvasnnpakrmafyalnsiepvigggsvkntlgyniknkseflsqyknfclensqgygyvte
kiidayfshtipiywgspsvaqdfnpksfvnvcdfkdfdaidhvrylhthpnayldmlyenplntldgkayfyqnlsfkk
ldffktilendtiyhdnpfiyrdlneplisiddlrnyddlrnyddlrnyddlrnyddlrnyddlrnyddlrnyddlrnyddlr
vnyddlrncddlrnyddlrnyerllqnaspllelsqnttfkiyrkayqkslpllaarklikklgl*

FIGURE 4

Fucosyltransferase strain 19C2 FutB nucleotide sequence (SEQ ID NO:7)

atgtccaaccctattagacgcttatatagacagcaccggttagatgaaaccgattataagccccattaaatatagccctagcg
aattgggtggcctttggataaaagagaaagcaaagggttagaaaaaaatttatcttacatttcattttaagtcagcattacacaatcgc
tctccaccgaaaccctgataaacctgcggacatcgttttgtaaccccttgatcagccagaaaaatcctatcctatcaaaacg
ctaaaagggtgtttacaccggtgaaaacgaagtcctaattcaacctcttgattacgcataggcttgatgaattggactttaga
gatcgttatttgagaatgcctttatattatgatagactacaccataaagccgagagcgtgaatgacaccaccgcaccttacaagatt
aaatctgacagcctttatgctttaaaaaagccctcccatcattttaagaaaaccacccacatttatgcgcgctaataataatgaga
tcgatcctttgaaaagaggggttgagcgtttgtcgcaagcaaccctaacgcccctataaggaacgctttctatgaggctttaattc
tattgagccagttactgggggagggagcgtgagaaacactttaggctataacgtcaaaaacaaaaacgaattttgagccaatac
aagttcaatctgtgctttgaaaacactcaaggctatggctatgttactgaaaaaatcattgacgcttactcagccacaccattcctat
ttattgggggggagtccttagcgtggcgaaagattttaacccc

Strain 19C2 FutB protein sequence (SEQ ID NO:8)

mfqplldayidstrldetdykpplnialanwwpldkreskgfrkkfilhflsqhytialhrmpdkpadivfgnplgsarkilsy
qnakrvfytgenevpnfnlfdyaigfdeldfrdrylrmplyydrllhkaesvndttapykiksdslyalkkpshhfkcnhph
lcalinneidplkrghasfvasnpnapimafyealnsiepvttgggsvmrlgynvknkneflsqyknlcfcntqgygyvtek
iidayfshtipiywggvpsvakdfnp

FIGURE 5

Strain 915 FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:9)

atggcctctaaatctccccctaaaaatcgctgtggcgaattggtggggagatgaagaaattaaaaattaaaaagagcgttct
ttattttatcctaagccagcattacacaatcactttacaccgaaaccctgataaacctgcggacatcgtctttgtaacccccttgat
cagccagaaaaatcttctatcaaaacgcaaaaagggtgtttacaccggtgaaatgaagtcctaacttcaacctcttgatta
cgccataggcttt

Protein sequence from Strain 915 FutA (SEQ ID NO:10)

maskspplkiavanwwgdeeikfkksvlyfilsqhytitlhrnpdkpadivfgnplgsarkilsyqnakrvfytgenevpn
fnlfdyaigf

FIGURE 6

Strain 26695 FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:11)

atgttccaaccctattagacgcctttatagaaagcgcttcattgaaaaaatggcctctaaatctccccccccccctaaaaatc
gctgtggcgaattggtggggagatgaagaaattaaagaatttaaaaagagcggtctttatcttaagccaacgctacgcaatc
accctccacaaaacccaatgaatttcagatctagtttttagcaatcctcttgagcggttagaaaagatttatcttaacaaacac
taaacgagtgttttacaccggtgaaaacgaatcacctaatttcaacctcttgattacgccataggcttgatgaattggatttaata
tcgttatttgagaatgcctttgtattatgccatttgactataaagccgagcttgtaatgacaccactgcgcctacaaactcaaag
acaacagcctttatgctttaaaaaaacccctctcatctttaaagaaaaccaccctaatttgcgcgtagtgaatgatgagagcg
atcttttaaaaagagggttgccagttttagcgagcaacgctaacgctcctatgaggaacgcttttatgacgctctaaattccata
gagccagttactgggggaggaagtgtgagaaacacttttaggctataaggttggaacaaaagcgagttttaagccaatacaagt
tcaatctctgtttgaaaactcgcaaggttatggctatgtaaccgaaaaaatccttgatgcgtatttagccataaccattcctatttg
ggggagtcccagcgtggcgaaagatttaaccctaaaagtttgaatgtgcatgattcaacaactttgatgaagcgattgattat
atcaaatacctgcacacgcacccaaacgcttatttagacatgctctatgaaaaccctttaaacacccttgatgggaaagcttacttt
accaagatttgagttttaaaaaaatcctagattttttaaaacgattttagaaaacgatacgatttatcacaattctcaacatcttcatg
tgggagtacgatctgcataagccgtagtatccattgatgattgagggttaattatgatgattgagggttaattatgaccggcttta
caaacgcttcgcctttattagaactctctcaaacaccacttttaaatctatcgcaaagcttatcaaaaatccttgcctttgttgcg
gcggtgagaaagtgggttaaaaattgggtttgtaa

Protein coding sequence Strain 26695 FutA (SEQ ID NO:12)

mfqplldafiesasiekmaskspppplkiavanwwgdeeikefkksvlyfilsqryaitlhqnpnefsdlvfnplgaarkil
syqntkrvfytgenespnfnldyaigfdeldfndrylrmplyyahlykaelvndttapyklkdnsllyalkkpsshhfenh
pnlcavvndesdlkrgfasfvasnanapmrnafydaalnsiepvttggsvmtlgykvgnksefilsqyknfncfensqgygy
vtekildayfshtipiywgspsvakdfnpksfvnvhdfnfdeaidyikylhthpnayldmlyenplntldgkayfyqdlf
kkildffktilendtiyhkfstsfmweydlhkplvsiddlrnyddlrnydrllqnaspllelsqnttfkiyrkayqkslpllav
rklvkkgl*

FIGURE 7

19C2A fucosyltransferase nucleotide sequence (SEQ ID NO:13)

atgtccaacccttactagacgcctttatagaaagtgtccaatt

19C2A predicted protein sequence (SEQ ID NO:14)

mfqplldafiesapi

FIGURE 8

Protein sequence from strain 1182 FutB aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

Query:	23	PPPLKIAVANWWGDEEVEEFKKNILYFILSQHYTITLHQNPNEPSDLVFGS-PIGSARKI	81
Sbjct:	11	TVPLLLAIYTWWSLIEYKEWKKSPIYFIGSQAPQPPLR---ILLWTWPFNGNPLALSDCP	67
Query:	82	LSYQNAKRVFYTGGEN---ESPNNLF---DYAIGFDELDFRDRYLRMPLYDYDRLHHKAES	135
Sbjct:	68	LSYQNTARCRLTANRSPLESADAVLFHHRDLSKGFDPDLPSPRPPGQPWVWASMESPSNS	127
Query:	136	-VNDTTSPIYKLPDLSYALKKPSHHFKENHPNLCAVVNNESEDPLKRGFASFVASNPN-AP	193
Sbjct:	128	GLNDLRDGYFNWTLSYRADSDAFHPYGYLEPRLSQVVNAPLLSAKRKGAAWVVSNCNTRS	187
Query:	194	KRNAFYDVLNSIEPVIGGGSVKNTLGYNINKKSEFLSQYKFNLCFENSQGYGYVTEKIID	253
Sbjct:	188	KRERFYKQLNKHQLQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKLWK	247
Query:	254	-AYFSHTIPIYWGSPSVAQDFNP-KSFVNVCDFKDFDEAIDHVRYLHTHPNAYL	305
Sbjct:	248	NALQAGTIPVVLGPRAYEDFVPPKSFIVHDDFKSPKELADYLLYLDTNPTAYS	301

FIGURE 9

Fucosyltransferase from strain 1111 FutA aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

Query:	27	I A V A N W G D E E I K F K K S V L Y F I L S Q H Y T I T L H R N P D K P A D I V F G - N P L G S A R K I L S Y Q N	
Sbjct:	16	L A I Y T W S L I E Y K E W K S P I Y F I G S Q A P Q P L R --- I L L W T W P F N G N P L A L S D C P L S Y Q N	85 72
Query:	86	A K R V F Y T G E N --- E V P N F N L F --- D Y A I G F D E L D F R D R Y L R M P L Y Y A Y L H Y K A E L - V N D T	138
Sbjct:	73	T A R C R L T A N R S P L E S A D A V L F H H R D L S K G F P D L P P S P R P P G Q P V W W A S M E S P S N S G L N D L	132
Query:	139	T S P Y K L Q P D S L Y A L K K P S H H F K E N H P N L C A V V N N E S D P L K R G F A S F V A S N P N - A P R R N A F	197
Sbjct:	133	R D G Y F N W T L S Y R A D S D A F H P Y G Y L E P R L S Q V V N A P L L S A K R K G A A W V V S N C N T R S K R E R F	192
Query:	198	Y E A L N A I E P V A G G G S V K N T L G Y N V K N K S E F L S Q Y K F N L C F E N T Q G Y G Y V T E K I I D - A Y F S	256
Sbjct:	193	Y K Q L N K H L Q V D V G G R V A N P L P L K V G C L V E T L S Q Y K F Y L A F E N S Q H Y D Y V T E K L W K N A L Q A	252
Query:	257	H T I P I Y W G S P S V A K D F N P - K S F V N V H D F N N F D E A I D Y I R Y L H T H P N A Y L D M H Y E N P L N T I	315
Sbjct:	253	G T I P V V L G P R A V Y E D F V P P K S F I H V D D F K S P K E L A D Y L L Y L D T N P T A Y S -----	301
Query:	316	D G K A Y F Y Q N L S F F K I L D F F K T I L E N D T I Y H D N P F I F Y R D L N E P S V S I D G L R V N Y D D L R V N	375
Sbjct:	302	----- E Y F E W R Y D L R V R L F S W D A L R -----	321
Query:	376	Y D D L R V N Y D D L R V N Y E R L L Q N A S P L L E L S Q N T T F K I Y R K A Y Q	417
Sbjct:	322	----- Y D E G F C R V C R L L Q N A P D ---- R Y K T Y P N I A K W F Q	351

FIGURE 10

Protein sequence from strain 1218 FutB aligned with pfam00852, Glyco_transf_10,
Glycosyltransferase family 10

Query:	23	PPPLKIAVANWWGDEEVEEFKKNILYFILSQHYTITLHQNPNEPSDLVFGS-PIGSARKI	81
Sbjct:	11	TVPLLLAIYTWWSLIEYKEWKKSPIYFIGSQAPQPPLR---ILLWTWPFNGNPLALSDCP	67
Query:	82	LSYQNAKRVFYTGGEN---ESPNFNLF---DYAIGFDELDFRDYLRMPLYYDRLHHKAES	135
Sbjct:	68	LSYQNTARCRLTANRSPLESADAVLFHHRDLSKGFDPDLPPSPRPPGQPWVWASMESPSNS	127
Query:	136	-VNDTTSPIYKLPDSLYALKKPSHHFKENHPNLCAVVNNESDPLKRGFASFVASNP-AP	193
Sbjct:	128	GLNDLRDGYFNWTLSYRADSDAFHPYGYLEPRLSQVVNAPLLSAKRKGAAWVVSNCNTRS	187
Query:	194	KRNAFYDALNSIEPVIGGGSVKNTLGYNIKNKSEFLSQYKFNLCFENSQGYGYVTEKIID	253
Sbjct:	188	KRERFYKQLNKHQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKLWK	247
Query:	254	-AYFSHTIPIYWGSPSVAQDFNP-KSFVNVCDFKDFDEAIDHVRYLHTHPNAYLDMLYEN	311
Sbjct:	248	NALQAGTIPVVLGPRAVYEDFVPPKSFIVDDFKSPKELADYLLYLDTNPTAYS-----	301
Query:	312	PLNTLDGKAYFYQNLSFKKILDFKTILENDTIYHDNPFIFYRDLNEPLISIDDLRVNYD	371
Sbjct:	302	-----EYFEWRYDLRVRLFSWDALR--YD	323
Query:	372	DLRVNYDDLVRVNYDDLVRVNYDDLVRVNYD	399
Sbjct:	324	EGFCRVCRLQNAPDRYKTYPNIAKWFQ	351

FIGURE 11

Protein sequence from strain 19C2 FutB aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

Query:	22	PPLNIALANWWPLDKRESKGFRKKFILHFILSQHYTIALHRNPDKPADIVFG-NPLGSAR	80
Sbjct:	12	VPLLLAIYTWWSL--IEYKEW-KKSPIYFIGSQAPQPPLR---ILLWTWPFNGNPLALSD	65
Query:	81	KILSYQNAKRVFYTGEN---EVPNFNLF---DYAIGFDELDFRDRYLRMPLYDYRLHHKA	134
Sbjct:	66	CPLSYQNTARCRLTANRSPLESADAVLFHHRDLSKGFPDLPPSPRPPGQPWWWASMESPS	125
Query:	135	ES-VNDTTAPYKIKSDSLYALKKPSHHFKENHPLCALINNEIDPLKRGFASFVASNP-	192
Sbjct:	126	NSGLNDLRDGYFNWTLSTYRADSDAFHPYGYLEPRLSQVVNAPLLSAKRKGAAWVVSNCNT	185
Query:	193	APIRNAFYEALNSIEPVTGGGSVRNTLGYNVKNKNEFLSQYKFNLCFENTQGYGYVTEKI	252
Sbjct:	186	RSKRERFYKQLNKHQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKL	245
Query:	253	ID-AYFSHTIPIYWGGVPSVAKDFNP	277
Sbjct:	246	WKNALQAGTIPVVLGP-RAVYEDFVP	270

FIGURE 12

	1		50
1111FutA.pep	(1)	MFQPLLDATIESAPKKWPLN--LPPLKIAVANWWGDEEKK--FKKS	
19C2A.pep	(1)	MFQPLLDATIESAPI-----	
915A.pepneose	(1)	-----MASK-SPPLKIAVANWWGDEEKK--FKKS	
26695A.pep	(1)	MFQPLLDATIESASIKMAKSPPPPLKIAVANWWGDEEKE--FKKS	
1182B.pep	(1)	MFQPLLDATIESASIKITKS-PPPLKIAVANWWGDEEKE--FKKN	
1218B.pep	(1)	MFQPLLDATIESASIKITKS-PPPLKIAVANWWGDEEKE--FKKN	
ORF19C2B.pep	(1)	MFQPLLDATIDSTRIDETDYK--PPLNTAIAVANWWPLDKRESKGRKKF	
Consensus	(1)	MFQPLLDATIESA IEK SK PPLKIAVANWWGDEEI FKK I	
	51		100
1111FutA.pep	(46)	LYFILSQHYTITLHRNPDKPADIVFGNPLGSARKILSYONAKRVFYTG	
19C2A.pep	(16)	-----	
915A.pepneose	(29)	LYFILSQHYTITLHRNPDKPADIVFGNPLGSARKILSYONAKRVFYTG	
26695A.pep	(48)	LYFILSQRYAITLHONPNEFEDIVFSNPLGSARKILSYONTKRVFYTG	
1182B.pep	(47)	LYFILSQHYTITLHONPNEFEDIVFGSPGSARKILSYONAKRVFYTG	
1218B.pep	(47)	LYFILSQHYTITLHONPNEFEDIVFGSPGSARKILSYONAKRVFYTG	
ORF19C2B.pep	(48)	LYFILSQHYTIALHRNPDKPADIVFGNPLGSARKILSYONAKRVFYTG	
Consensus	(51)	LYFILSQHYTITLH NP PADIVFGNPLGSARKILSYONAKRVFYTG	
	101		150
1111FutA.pep	(96)	EVPNFNLFDYAIGFDELDFRDRYLRMPLYAYLHKAELVNDTTSPYKLQ	
19C2A.pep	(16)	-----	
915A.pepneose	(79)	EVPNFNLFDYAIGF-----	
26695A.pep	(98)	ESPNFNLFDYAIGFDELDFNDRYLRMPLYAHLHKAELVNDTTSPYKLK	
1182B.pep	(97)	ESPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHKAESVNDTTSPYKLK	
1218B.pep	(97)	ESPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHKAESVNDTTSPYKLK	
ORF19C2B.pep	(98)	EVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHKAESVNDTTSPYKLK	
Consensus	(101)	E PNFNLFDYAIGFDELDFRDRYLRMPLY LHHKAE VNDTTSPYKLK	
	151		200
1111FutA.pep	(146)	PDSLIALKKPSHHFKENHPNLCVVNNESDPLKRGFASFVASNPNAPRRN	
19C2A.pep	(16)	-----	
915A.pepneose	(93)	-----	
26695A.pep	(148)	DNSIALKKPSHHFKENHPNLCVVNDEEDLLKRGFASFVASNANAPMRN	
1182B.pep	(147)	PDSLIALKKPSHHFKENHPNLCVVNNESDPLKRGFASFVASNPNAPKRN	
1218B.pep	(147)	PDSLIALKKPSHHFKENHPNLCVVNNESDPLKRGFASFVASNPNAPKRN	
ORF19C2B.pep	(148)	SDSLIALKKPSHHFKENHPNLCALNNEIDPLKRGFASFVASNPNAPIRN	
Consensus	(151)	DSLIALKKPSHHFKENHPNLCVVNNESDPLKRGFASFVASNPNAP RN	
	201		250
1111FutA.pep	(196)	AFYDALNSIEPVACGGSVNTLGYNKNKSEFLSQYKFNLCFENTOGYGY	
19C2A.pep	(16)	-----	
915A.pepneose	(93)	-----	
26695A.pep	(198)	AFYDALNSIEPVTCGGSVNTLGYKGNKSEFLSQYKFNLCFENSOGYGY	
1182B.pep	(197)	AFYDALNSIEPVIGGGSVNTLGYNKNKSEFLSQYKFNLCFENSOGYGY	
1218B.pep	(197)	AFYDALNSIEPVIGGGSVNTLGYNKNKSEFLSQYKFNLCFENSOGYGY	
ORF19C2B.pep	(198)	AFYDALNSIEPVTCGGSVNTLGYNKNKSEFLSQYKFNLCFENTOGYGY	
Consensus	(201)	AFYDALNSIEPV GGGSVNTLGYNVKNKSEFLSQYKFNLCFENSOGYGY	

	1	50
1111FutA	(1) ATGTTCCAACCCCTATTAGATGCCTTTATAGAAAGCGCT-CCATTGAAAA	
915A.cod (MWG)	(1) ATGTTCCAACCCCTATTAGATGCCTTTATAGAAAGCGCTTCCATTGAAAA	
19C2FutA.cod	(1) ATGTTCCAACCCCTTACTAGACGCCTTTATAGAAAGTGCTCCAATT-----	
26695A.cod	(1) ATGTTCCAACCCCTATTAGACGCCTTTATAGAAAGCGCTTCCATTGAAAA	
1182B	(1) ATGTTCCAACCCCTATTAGACGCCTTATATAGAAAGCGCTTCCATTGAAAA	
1218B.nuc	(1) ATGTTCCAACCCCTATTAGACGCCTTATATAGAAAGCGCTTCCATTGAAAA	
ORF19C2B	(1) ATGTTCCAACCCCTATTAGACGCCTTATATAGACAGCACCCGTTTAGATGA	
Consensus	(1) ATGTTCCAACCCCTATTAGACGCCTTTATAGAAAGCGCTTCCATTGAAAA	
	51	100
1111FutA	(50) AATGGCCTCTAAATCTCCCCCCCC-----TAAAAATCGCTGTGGCGAATT	
915A.cod (MWG)	(51) AATGGCCTCTAAATCTCCCCCCCC-----TAAAAATCGCTGTGGCGAATT	
19C2FutA.cod	(46) -----	
26695A.cod	(51) AATGGCCTCTAAATCTCCCCCCCCCCCCCTAAAAATCGCTGTGGCGAATT	
1182B	(51) AATTACCTCTAAATCTCCCCCCCC-----TAAAAATCGCTGTGGCGAATT	
1218B.nuc	(51) AATTACCTCTAAATCTCCCCCCCC-----TAAAAATCGCTGTGGCGAATT	
ORF19C2B	(51) AACCGATTATAA-----GCCCCCAT---TAAATATAGCCCTAGCGAATT	
Consensus	(51) AAT GCCTCTAAATCTCCCCCCCC TAAAAATCGCTGTGGCGAATT	
	101	150
1111FutA	(95) GGTGG-----GGAGATGA-AGAAATTAAAAAATTTAAAAAGAGCGTTCTT	
915A.cod (MWG)	(95) GGTGG-----GGAGATGA-AGAAATTAAAAAATTTAAAAAGAGCGTTCTT	
19C2FutA.cod	(46) -----	
26695A.cod	(101) GGTGG-----GGAGATGA-AGAAATTAAAGAATTTAAAAAGAGCGTTCTT	
1182B	(98) GGTGG-----GGAGATGA-AGAGGTTGAAGAATTTAAAAAGAACATTCTT	
1218B.nuc	(98) GGTGG-----GGAGATGA-AGAGGTTGAAGAATTTAAAAAGAACATTCTT	
ORF19C2B	(92) GGTGGCCTTTGGATAAAAGAGAAAGCAAAGGGTTTAGAAAAAATTTATC	
Consensus	(101) GGTGG GGAGATGA AGAAATTAAAGAATTTAAAAAGA C TTCTT	
	151	200
1111FutA	(139) T---ATTTTATCCTAAGCCAGCATTACACAATCACTTTACACCGAAACCC	
915A.cod (MWG)	(139) T---ATTTTATCCTAAGCCAGCATTACACAATCACTTTACACCGAAACCC	
19C2FutA.cod	(46) -----	
26695A.cod	(145) T---ATTTTATCCTAAGCCAACGCTACGCAATCACCTTGCACCAAAACCC	
1182B	(142) T---ATTTTATTCTCAGTCAGCATTACACAATCACCTTGCACCAAAACCC	
1218B.nuc	(142) T---ATTTTATTCTCAGTCAGCATTACACAATCACCTTGCACCAAAACCC	
ORF19C2B	(142) TTACATTTCAATTTAAGTCAGCATTACACAATCGCTCTCCACCGAAACCC	
Consensus	(151) T ATTTTAT CTAAG CAGCATTACACAATCAC CTCCACC AAACCC	
	201	250
1111FutA	(186) TGATAAACCTGCGGACATCGTCTTTGGTAACCCCTTGGATCAGCCAGAA	
915A.cod (MWG)	(186) TGATAAACCTGCGGACATCGTCTTTGGTAACCCCTTGGATCAGCCAGAA	
19C2FutA.cod	(46) -----	
26695A.cod	(192) CAATGAATTTTCAGATCTAGTTTTTAGCAATCCTCTTGGAGCGGCTAGAA	
1182B	(189) CAACGAACCTCCGATCTCGTCTTTGGCAGTCCTATTGGATCAGCCAGAA	
1218B.nuc	(189) CAACGAACCTCCGATCTCGTCTTTGGCAGTCCTATTGGATCAGCCAGAA	
ORF19C2B	(192) TGATAAACCTGCGGACATCGTTTTTTGGTAACCCCTTGGATCAGCCAGAA	
Consensus	(201) AT AACCT C GA TCGTCTTTGG AA CC CTTGGATCAGCCAGAA	

FIG. 13 (1/6)

	251	300
1111FutA	(236) AAATCTTATCCTATCAAAAACGCAAAAAGGGTGTGTTTACACCGGTGAAAAT	
915A.cod (MWG)	(236) AAATCTTATCCTATCAAAAACGCAAAAAGGGTGTGTTTACACCGGTGAAAAT	
19C2FutA.cod	(46) -----	
26695A.cod	(242) AGATTTTATCTTATCAAAAACACTAAACGAGTGTGTTTACACCGGTGAAAAC	
1182B	(239) AAATCTTATCCTATCAAAAACGCAAAAAGAGTGTGTTTACACCGGTGAAAAC	
1218B.nuc	(239) AAATCTTATCCTATCAAAAACGCAAAAAGAGTGTGTTTACACCGGTGAAAAC	
ORF19C2B	(242) AAATCCTATCCTATCAAAAACGCTAAAAGGGTGTGTTTACACCGGTGAAAAC	
Consensus	(251) AAATCTTATCCTATCAAAAACGCAAAAAG GTGTTTACACCGGTGAAAAC	
	301	350
1111FutA	(286) GAAGTCCCTAACTTCAACCTCTTTGATTACGCCATAGGCTTT -GATGAAT	
915A.cod (MWG)	(286) GAAGTCCCTAACTTCAACCTCTTTGATTACGCCATAGGCTTTTGATGA - -	
19C2FutA.cod	(46) -----	
26695A.cod	(292) GAATCACCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT -GATGAAT	
1182B	(289) GAATCGCCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT -GATGAAT	
1218B.nuc	(289) GAATCGCCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT -GATGAAT	
ORF19C2B	(292) GAAGTCCCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT -GATGAAT	
Consensus	(301) GAA CCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT GATGAAT	
	351	400
1111FutA	(335) TGGACTTTAGAGATCGTTATTTGAGAATGCCTTTGTATTATGCCTATTTG	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(341) TGGATTTTAATGATCGTTATTTGAGAATGCCTTTGTATTATGCCCATTTG	
1182B	(338) TGGATTTTAGAGATCGTTATTTAAGAATGCCTTTATATTATGATAGACTA	
1218B.nuc	(338) TGGATTTTAGAGATCGTTATTTAAGAATGCCTTTATATTATGATAGACTA	
ORF19C2B	(341) TGGACTTTAGAGATCGTTATTTGAGAATGCCTTTATATTATGATAGACTA	
Consensus	(351) TGGA TTTAGAGATCGTTATTT AGAATGCCTTT TATTATG T	
	401	450
1111FutA	(385) CATTATAAAGCCGAGCTTGTTAATGACACCACTTCGCCTTATAAACTCCA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(391) CACTATAAAGCCGAGCTTGTTAATGACACCACTTCGCCTTACAAACTCAA	
1182B	(388) CACCATAAAGCCGAGAGCGTGAATGACACCACTTCGCCTTACAAACTCAA	
1218B.nuc	(388) CACCATAAAGCCGAGAGCGTGAATGACACCACTTCGCCTTACAAACTCAA	
ORF19C2B	(391) CACCATAAAGCCGAGAGCGTGAATGACACCACTTCGCCTTACAAAGATTAA	
Consensus	(401) CAC ATAAAGCCGAG GT AATGACACCACT CGCCTTACAAACTCAA	
	451	500
1111FutA	(435) ACCTGACAGCCTTTATGCTTTAAAAAAAGCCCTCCCATCATTTTAAAGAAA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(441) AGACAACAGCCTTTATGCTTTAAAAAAAGCCCTCTCATCATTTTAAAGAAA	
1182B	(438) ACCTGACAGCCTTTATGCTTTAAAAAAAGCCCTCCCATCATTTTAAAGAAA	
1218B.nuc	(438) ACCTGACAGCCTTTATGCTTTAAAAAAAGCCCTCCCATCATTTTAAAGAAA	
ORF19C2B	(441) ATCTGACAGCCTTTATGCTTTAAAAAAAGCCCTCCCATCATTTTAAAGAAA	
Consensus	(451) A CTGACAGCCTTTATGCTTTAAAAAAAGCCCTCCCATCATTTTAAAGAAA	

FIG. 13 (2/6)

	501	550
1111FutA	(485) ACCACCCCAATTTGTGCGCAGTAGTGAATAATGAGAGTGATCCTTTGAAA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(491) ACCACCCTAATTTGTGCGCAGTAGTGAATGATGAGAGCGATCTTTTAAAA	
1182B	(488) ACCACCCCAATTTATGCGCAGTAGTGAACAATGAGAGCGATCCTTTGAAA	
1218B.nuc	(488) ACCACCCCAATTTATGCGCAGTAGTGAACAATGAGAGCGATCCTTTGAAA	
ORF19C2B	(491) ACCACCACATTTATGCGCGCTAATCAATAATGAGATCGATCCTTTGAAA	
Consensus	(501) ACCACCC AATTT TGCGCAGTAGTGAA AATGAGAGCGATCCTTTGAAA	
	551	600
1111FutA	(535) AGAGGGTTTGCAGCTTTGTGCGCAAGCAACCCTAACGCTCCTAGAAAGGAA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(541) AGAGGGTTTGCAGTTTTGTAGCGAGCAACGCTAACGCTCCTATGAGGAA	
1182B	(538) AGAGGGTTTGCAGTTTTGTAGCGAGCAACCCTAACGCTCCTAAAAGGAA	
1218B.nuc	(538) AGAGGGTTTGCAGTTTTGTAGCGAGCAACCCTAACGCTCCTAAAAGGAA	
ORF19C2B	(541) AGAGGGTTTGCAGCTTTGTGCGCAAGCAACCCTAACGCCCCATATAAGGAA	
Consensus	(551) AGAGGGTTTGCAG TTTGT GC AGCAACCCTAACGCTCCTA AAGGAA	
	601	650
1111FutA	(585) CGCTTTTTATGAGGCTTTTAAACGCTATTGAGCCAGTTGCTGGGGGAGGGA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(591) CGCTTTTTATGACGCTCTAAATTCCATAGAGCCAGTTACTGGGGGAGGAA	
1182B	(588) TGCTTTCTATGACGTTTTTAAATTCTATAGAGCCAGTTATTGGGGGAGGGA	
1218B.nuc	(588) TGCTTTCTATGACGCTTTTAAATTCTATAGAGCCAGTTATTGGGGGAGGGA	
ORF19C2B	(591) CGCTTTCTATGAGGCTTTTAAATTCTATTGAGCCAGTTACTGGGGGAGGGA	
Consensus	(601) GCTTT TATGA GCTTTAAATTCTAT GAGCCAGTTA TGGGGGAGGGA	
	651	700
1111FutA	(635) GCGTGAAAAACACTTTAGGCTATAATGTCAAAAACAAGAGCGAGTTTTTA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(641) GTGTGAGAAACACTTTAGGCTATAAGGTTGGAACAAAAGCGAGTTTTTA	
1182B	(638) GCGTGAAAAACACTTTAGGCTATAACATTAAAAACAAGAGCGAGTTTTTA	
1218B.nuc	(638) GCGTGAAAAACACTTTAGGCTATAACATTAAAAACAAGAGCGAGTTTTTA	
ORF19C2B	(641) GCGTGAGAAACACTTTAGGCTATAACGTCAAAAACAACGAATTTTTG	
Consensus	(651) GCGTGA AAACACTTTAGGCTATAA T AAAAACAA AGCGAGTTTTTA	
	701	750
1111FutA	(685) AGCCAATACAAATTCAATCTGTGTTTTGAAAACACTCAAGGCTATGGCTA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(691) AGCCAATACAAGTTCAATCTCTGTTTTGAAAACCTCGCAAGGTTATGGCTA	
1182B	(688) AGCCAATACAAATTCAATCTGTGTTTTGAAAACCTCACAAGGCTATGGCTA	
1218B.nuc	(688) AGCCAATACAAATTCAATCTGTGTTTTGAAAACCTCACAAGGCTATGGCTA	
ORF19C2B	(691) AGCCAATACAAGTTCAATCTGTGCTTTGAAAACACTCAAGGCTATGGCTA	
Consensus	(701) AGCCAATACAA TTCAATCTGTGTTTTGAAAAC C CAAGGCTATGGCTA	

FIG. 13 (3/6)

	751	800
1111FutA	(735)	TGTAACCTGAAAAGATCATTGACGCTTATTTTCAGCCATACCATTTCCTATTT
915A.cod (MWG)	(334)	-----
19C2FutA.cod	(46)	-----
26695A.cod	(741)	TGTAACCGAAAAAATCCTTGATGCGTATTTTAGCCATACCATTTCCTATTT
1182B	(738)	TGTAACCTGAAAAAATCATTGACGCTTACTTTAGCCATACCATTTCCTATTT
1218B.nuc	(738)	TGTAACCTGAAAAAATCATTGACGCTTACTTTAGCCATACCATTTCCTATTT
ORF19C2B	(741)	TGTTACTGAAAAAATCATTGACGCTTACTTCAGCCACACCATTCCTATTT
Consensus	(751)	TGTAACCTGAAAAAATCATTGACGCTTA TT AGCCATACCATTTCCTATTT
	801	850
1111FutA	(785)	ATTGGGGG--AGTCC-CAGCGTGGCGAAAGATTTTAACCCTAAGAGTTTT
915A.cod (MWG)	(334)	-----
19C2FutA.cod	(46)	-----
26695A.cod	(791)	ATTGGGGG--AGTCC-CAGCGTGGCGAAAGATTTTAACCCTAAGAGTTTT
1182B	(788)	ATTGGGGG--AGTCC-TAGCGTGGCGACAAGATTTTAAGCCTAAGAGTTTT
1218B.nuc	(788)	ATTGGGGG--AGTCC-TAGCGTGGCGACAAGATTTTAACCCTAAGAGTTTT
ORF19C2B	(791)	ATTGGGGGGGAGTCCCTAGCGTGGCGAAAGATTTTAACCCC-----
Consensus	(801)	ATTGGGGG AGTCC AGCGTGGC AAGATTTTAACCCTAA AGTTTT
	851	900
1111FutA	(832)	GTGAATGTCCATGATTTCAACAACCTTGATGAAGCGATTGACTATATCAG
915A.cod (MWG)	(334)	-----
19C2FutA.cod	(46)	-----
26695A.cod	(838)	GTGAATGTGCATGATTTCAACAACCTTGATGAAGCGATTGATTATATCAA
1182B	(835)	GTGAATGTTTGTGATTTTAAAGATTTTGATGAAGCGATTGATCATGTGCG
1218B.nuc	(835)	GTGAATGTTTGTGATTTTAAAGATTTTGATGAAGCGATTGATCATGTGCG
ORF19C2B	(832)	-----
Consensus	(851)	GTGAATGT TGATTT AA A TTTGATGAAGCGATTGA AT T
	901	950
1111FutA	(882)	ATACTTGACACACGCACCCAAACGCTTATTTAGACATGCACTATGAAAACC
915A.cod (MWG)	(334)	-----
19C2FutA.cod	(46)	-----
26695A.cod	(888)	ATACCTGCACACGCACCCAAACGCTTATTTAGACATGCTCTATGAAAACC
1182B	(885)	ATACTTGACACACGCACCCAAACGCTTATTTAGACATGCTTTATGAAAACC
1218B.nuc	(885)	ATACTTGACACACGCACCCAAACGCTTATTTAGACATGCTTTATGAAAACC
ORF19C2B	(832)	-----
Consensus	(901)	ATAC TGCACACGCACCCAAACGCTTATTTAGACATGC TATGAAAACC
	951	1000
1111FutA	(932)	CTTTAAACACTATTGATGGGAAAGCTTACTTTTACCAAATTTGAGTTTT
915A.cod (MWG)	(334)	-----
19C2FutA.cod	(46)	-----
26695A.cod	(938)	CTTTAAACACCCTTGATGGGAAAGCTTACTTTTACCAAAGATTGAGTTTT
1182B	(935)	CTTTAAACACCCTTGATGGGAAAGCTTACTTTTACCAAATTTGAGTTTT
1218B.nuc	(935)	CTTTAAACACCCTTGATGGGAAAGCTTACTTTTACCAAATTTGAGTTTT
ORF19C2B	(832)	-----
Consensus	(951)	CTTTAAACAC TTGATGGGAAAGCTTACTTTTACCAA ATTTGAGTTTT

FIG. 13 (4/6)

		1001		1050
1111FutA	(982)	AAAAAAATCCTAGATTTTTTTTAAAACGATTTTAGAAAACGACACGATCTA		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(988)	AAAAAAATCCTAGATTTTTTTTAAAACGATTTTAGAAAACGATACGATTTA		
1182B	(985)	AAAAAAATCCTAGATTTTTTTTAAAACGATTTTAGAAAACGACACGATTTA		
1218B.nuc	(985)	AAAAAAATCCTAGATTTTTTTTAAAACGATCTTAGAAAACGACACGATTTA		
ORF19C2B	(832)	-----		
Consensus	(1001)	AAAAAAATCCTAGATTTTTTTTAAAACGAT TTAGAAAACGA ACGAT TA		
		1051		1100
1111FutA	(1032)	TCACGATAACCC-----TTTCATTTTCTATCGTGATTGGAATGAGCCCTT		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1038)	TCACAAATTCTCAACATCTTTTCATGTGGGAGTACGATCTGCATAAGCCGT		
1182B	(1035)	TCACGATAACCC-----TTTTATTTTTCATCGTGATTGGAATGAGCCGT		
1218B.nuc	(1035)	TCACGATAACCC-----TTTTATTTTTCATCGTGATTGGAATGAGCCGT		
ORF19C2B	(832)	-----		
Consensus	(1051)	TCAC A C C TTT AT T A GAT TG AT AGCC T		
		1101		1150
1111FutA	(1076)	CAGTATCTATTGATGGT---TTGAGGGTTAATTATGATGATTTGAGGGTT		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1088)	TAGTATCCATTGATGAT---TTGAGGGTTAATTATGATGATTTGAGGGTT		
1182B	(1079)	TAATATCTATTGATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTT		
1218B.nuc	(1079)	TAATATCTATTGATGAT---TTGAGGGTTAATTATGATGATTTGAGGGTT		
ORF19C2B	(832)	-----		
Consensus	(1101)	A TATC ATTGATG T TTGAGGGTTAATTATGATGATTTGAGGGTT		
		1151		1200
1111FutA	(1123)	AATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGA		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1135)	AATTATGACCGGCTTTTACAAAACGCTTCGCCTTTATTAGAACTCTCTCA		
1182B	(1129)	AATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGA		
1218B.nuc	(1126)	AATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGA		
ORF19C2B	(832)	-----		
Consensus	(1151)	AATTATGA T AA T TTT G T T A		
		1201		1250
1111FutA	(1173)	GCGCCTTTTACAAAACGCTCGCCTTTATTAGAACTCTCTCAAAACACCA		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1185)	AAACACCACTTTTAAAATCTATCGCAAAGCTTATCAAAAATCCTTGCCCTT		
1182B	(1179)	TGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGA		
1218B.nuc	(1176)	TGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGA		
ORF19C2B	(832)	-----		
Consensus	(1201)	AA		

FIG. 13 (5/6)

		1251	1300
1111FutA	(1223)	CTTTTAAAATCTATCGCAAAGCTTATCAAAAATCCTTGCCTTTGTTGCGT	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1235)	TGTTGCGCGCGGTGAGAAAAGTTGGTTAAAAAATTGGGTTTGTA-----	
1182B	(1229)	GGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAAT	
1218B.nuc	(1226)	GGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAAT	
ORF19C2B	(832)	-----	
Consensus	(1251)	T	T A A
		1301	1350
1111FutA	(1273)	GCCATAAGGAGATGGGTTAAAAAGTAA-----	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1279)	-----	
1182B	(1279)	TATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGAGCG	
1218B.nuc	(1276)	TGTGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGAGCG	
ORF19C2B	(832)	-----	
Consensus	(1301)		
		1351	1400
1111FutA	(1300)	-----	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1279)	-----	
1182B	(1329)	GCTCTTACAAAACGCCTCGCCTTTATTAGAACTCTCTCAAAACACCACTT	
1218B.nuc	(1326)	GCTCTTACAAAACGCCTCGCCTTTATTAGAACTCTCTCAAAACACCACTT	
ORF19C2B	(832)	-----	
Consensus	(1351)		
		1401	1450
1111FutA	(1300)	-----	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1279)	-----	
1182B	(1379)	TTAAATCTATCGCAAAGCTTATCAAAAATCCTTACCTTTGTTGCGTGCG	
1218B.nuc	(1376)	TTAAATCTATCGCAAAGCTTATCAAAAATCCTTACCTTTGTTGCGTGCG	
ORF19C2B	(832)	-----	
Consensus	(1401)		
		1451	1483
1111FutA	(1300)	-----	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1279)	-----	
1182B	(1429)	GCGAGAAAAGTTGATTAAAAAATTGGGTTTGTA	
1218B.nuc	(1426)	GCGAGAAAAGTTGATTAAAAAATTGGGTTTGTA	
ORF19C2B	(832)	-----	
Consensus	(1451)		

FIG. 13 (6/6)

Oligo Structures

Lacto-N-neo-Tetraose (LNnT)



Lacto-N-Fucopentaose III (LNFP III)



3



1 α Fucose

FIG. 14

Linkage Analysis by GC/MS

The samples were methylated, hydrolyzed, reduced with sodium borodeuteride, acetylated and analyzed by GC/MS along with samples of LNT and LNF3.

- ▶ A Glc vs. Glc-NAc value close to 1 favors fucosylation of Glc-NAc.
- ▶ A Glc vs. Glc-NAc value close to 0 favors fucosylation of Glc

<i>H. Pylori</i> Strain	Glc vs. Glc-NAc
915A2	0.982
19C2A5	0.040
1111A2	0.975
19C2B1	0.991
1182B3	0.983

FIG. 15

1 Liter LNFIII Synthesis

Batch Number	Resin Type	Total Yield	Actual Percent Recovery
1-02	MR3 NH_4HCO_3 column (1ml resin/1ml synthesis)	1.567 g	61%
2-02	MR3 NH_4HCO_3 column (1ml resin/1ml synthesis)	1.760 g	68%
3-02	Dowex1/Dowex 50 (2ml resin/1ml synthesis)	1.221 g	47%

FIG. 16

FIG. 17

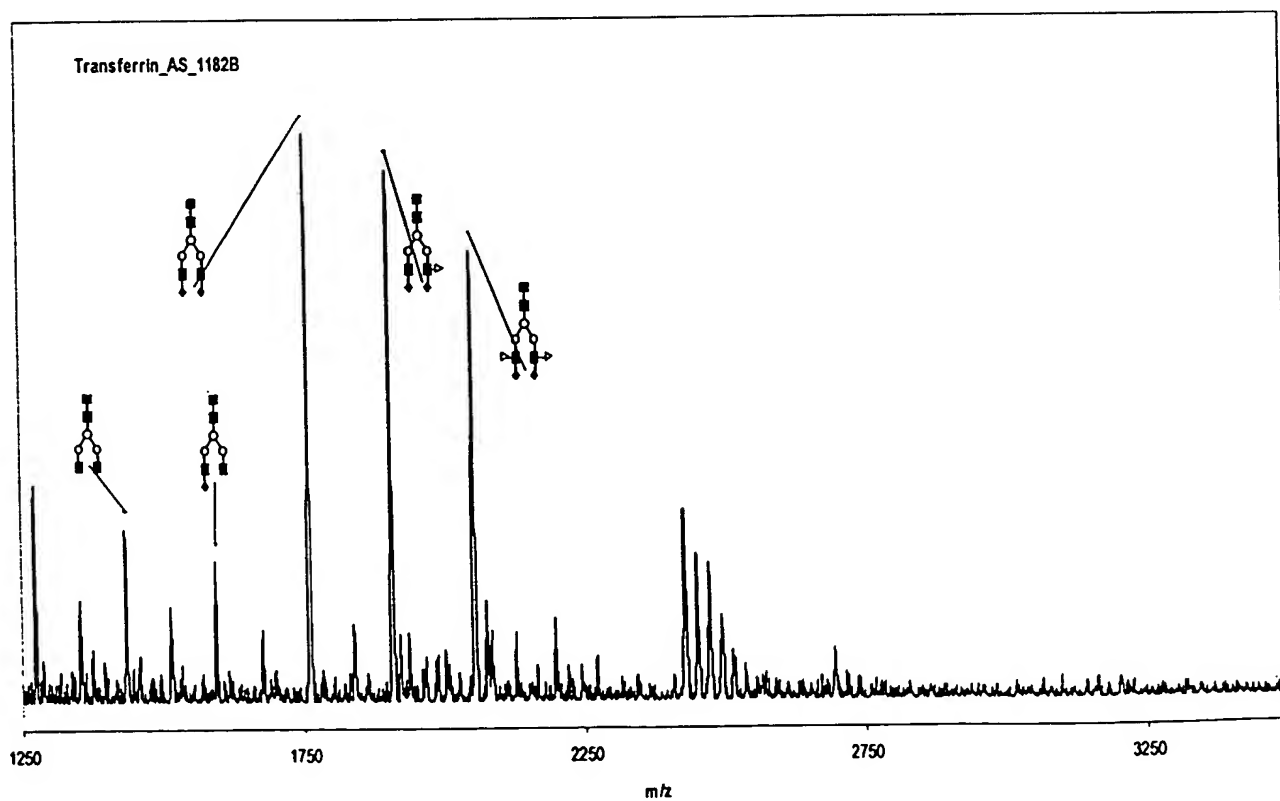
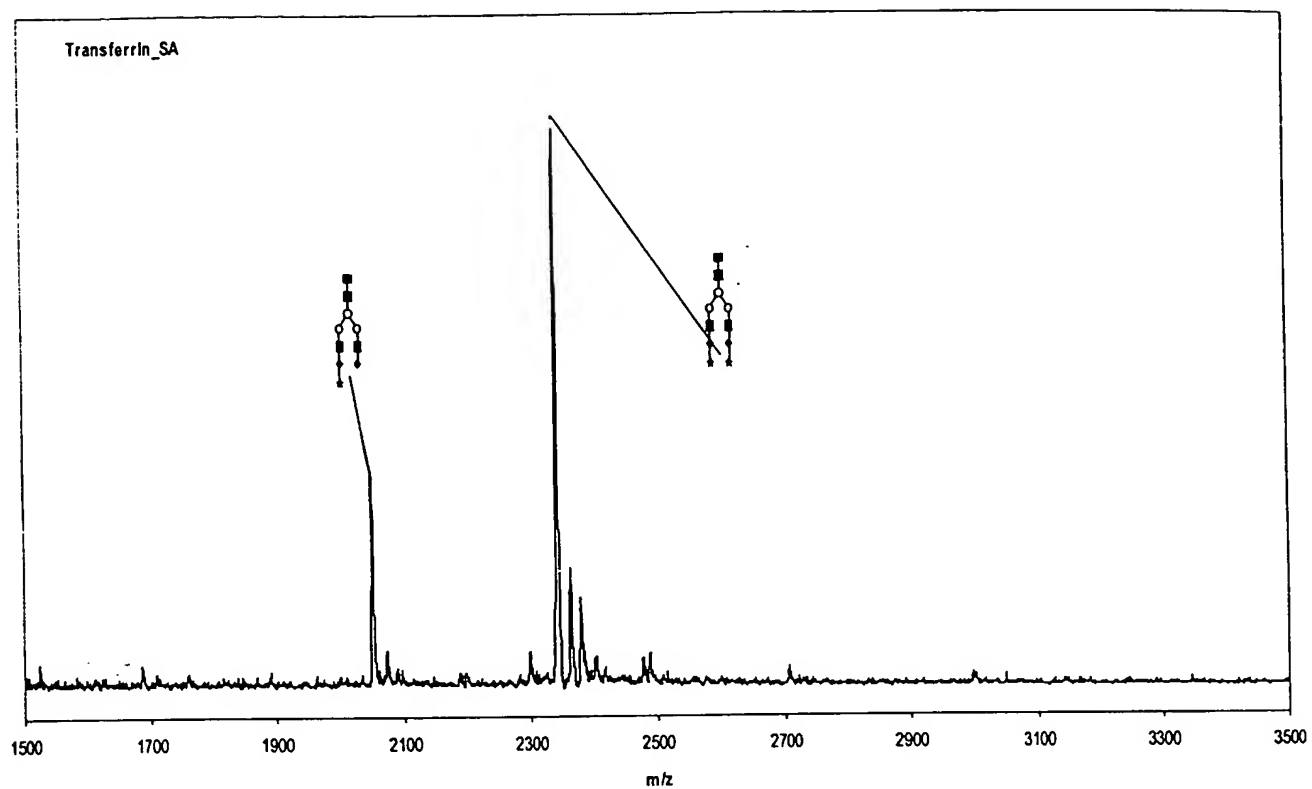


FIGURE 18

Strain 1111FutB fucosyltransferase nucleotide coding sequence (SEQ ID NO:15)

ggatccCGAGCGACCAATCATTACAGGGATTTATTGCATTTAGATGCGGCTTTTCAGTAACACGCTGATCGT
GGAAAATAACGCCTTAAACGGCTTGGTTACCGGGCATATGATGTTTTTCACATTCTAAAGGCGAAATGCTCC
TCGCTTTGCAACGCTCGTTGAATATCAGTAAAGATCGCACCTTTAGTCGTGGGCGATGGGGCGAATGATTG
AGCATGTTCAAACATGCCCATATTAATAATCGCTTTCACGCTAAAGAGGTTTTAAACAGCACGCCACGCA
TTGCATCAATGAGCCTAATCTAGCCCTAATCAAGCCTTTGATTTACAAAAATTTTTTTTGTAAAAATCCCT
TTAAAAGGATAGCCatggttccaacccctattagacgcttatgtagaaagcgcttcattgaaaaaatggcc
tctaaatctccccccccccctaaaaatcgctgtggcgaaattggtggggagatgaagaaattaaagaatttaa
aaagagcggtctttatcttttagccaacgctacacaatcgccctccacccaaaccccaatgaatttt
cagatctagtccttagcaatcctcttggtacgctagaaaaatcttatcgctatcaaaacgctaaaagagt
ttttacaccggtgaaaatgaagtccttaacttcaacctctttgattacgccataggctttgatgaattgga
ttttagagatcggtatttgaggatgcctttatattatgataggctacaccataaagccgagagcggtgaatg
acaccacttcgccctacaaactcaaagacaacagcctttatactttaaaaaaacccctcccatcaatttaa
gaaaaccaccctaattttagcgcagtcgtgaatgatgagagcgatcctttgaaaagaggggttgtagccttt
gtagcgagcaacgctaacgctcctatgagaaacgccttttatgacgctttaaattctattgagccagttac
tgggggagggagcggtgaaaaacactttaggctataacgtcaaaaacaagagcgagtttttaagccaataca
agttcaacctgtgttttgaaaactcacaaggctatggctatgtaaccgagaagatccttgacgcttacttt
agccacaccattcctattttatgggggagtccttagcgtggcgaaagatttttaaccctaaagagtttgtaa
tgtccatgatttcaacaactttgatgaagcgatagattatatcaaatacttgacacgcacccaaacgctt
atttagacatgctctatgaaaacccctttaaacgccttgatgggaaagcttacttttaccaggatttgagt
tttaaaaaaatcctagctttttttaaacgatttttagaaaacgatacgatttatcacaatcctcaacatc
tttcatgtggagtgcatctcgatgagccggttagcgtctattgatgatttgagggttaattatgatgattt
gagggttaattatgatgatttgagggttaattatgatgatttgagggttaattatgatgatttgagggtta
attatgatgatttgagggttaattatagcgcttttgcaaacgcttcacctttattggaattatcccaaa
acacctcttttaaaatctatcgcaaagcctatcaaagcctatcaaaaatccttacccttattgcgcgccat
aaGGAGATGGGTTAAAAAGTAAGGTGTCTTTTAAGACTGGTTGAGAAATTGAAGCGCTATTTTAAATGCG
CTAACGCTTCTTTTTTGAGCGTGGGGTTTTTGAGCATGTCCTCTAAAGCATGGGCGCTTAAAAATGTTTG
GATTTTAAAGACACGATGCGCCCAAAGGATTCTTCTTTAGAAAAGGTTTAAAGGCGTTTGGGCAAAATCTC
GCCAAATACGATAATGACTTTTGAAGCGCTGTTGTCTAATTGCCAGGTCGgaattc

Strain 1111FutB fucosyltransferase amino acid sequence (SEQ ID NO:16)

MFQPLLDAYVESASIEKMASKSPPLKIAVANWWGDEEIKEFKKSVLYFIFSQRYTIALHQNPNEFSDLVF
SNPLGSARKILSYQNAKRVFYTGNEVPNFNLFDYAIGFDELDFRDRYLRLPLYDRLHHKAESVNDTTSP
YKLDNSLYTLKKPSHQFKENHPNLCAVVNDESPLKRGVVSFVASNANAPMRNAFYDALNSIEPVTGGGS
VKNTLGYNVKNKSEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDF
NNFDEAIDYIKYLHTHPNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFFKTI LENDTIYHKSSTSMWE
CDLDEPLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQNTSF
KIYRKAYQKPIKNPYPCAP

FIGURE 19

Strain 802FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:17)

ggatccCGGCGTGAATTACTACCTTTCTGGCTTGCACAGCTATGCCGCAGGCGATCCCTTGCCTATCCCTA
CTTTCTTATACTTTTGGTAGCGATACCTTTTGCTCTCGTGATTTTGGCTTATTTCAAACGCCATTTGAGT
TTGCCTAAATTGGTTTAAAGGATAGCCatgTTCAGCCCTTACTAGACGCCCTTTATAGAAAGTGCTTCAAT
TAAAAAATGCCTCTGAGTTACCCCCCCCATAAAATCGCTGTGGCGAATTGGTGGGGAGGCGCTGAAGAAT
TTAAAAAGAGCGCTATGTATTTTCATCCTAAGCCAACGCTACACAATCACCTCCACCAAACCCCAACGAA
CCCTCCGATCTCGTCTTTGGCAGTCCTATTGGAGCAGCCAGAAAAATCCTATCCTACCAAACACTAAAAG
AGTGTTTTACGCCGGTGAAAATGAAGTCCCTAATTTCAACCTCTTTGATTACGCCATAGGCTTTGATGAAT
TGGATTTTAGAGATCGTTATTTGAGAATGCCTTTATATTATGATAGACTACACCATAAAGCCGAGAGCGTG
AATGACACCACCGCGCCTTACAAGATTAAACCTGACAGCCTTTATACTTTAAAAAAACCTCCCATCATTT
TAAAGAAAAACACCCCATTTATGCGCAGTAGTGAATGATGAGAGCGATCCTTTGAAAAGAGGGTTTGCGA
GTTTTGTGCGCAAGCAACCCTAACGCTCCTAAAAGGAACGCCTTCTATGACGCTTTAAATTCTATTGAGCCA
GTTACTGGGGGAGGGAGCGTGAAAAACACTTTAGGCTATAAAGTTGGAACAAAAACGAGTTTTTAAAGCCA
ATACAAATTCAATCTGTGTTTTGAAAACCTCAAGGCTATGGCTATGTAACCGAAAAAATCATTGACGCTT
ACTTTAGCCATACCATTCCTATTTATTGGGGGAGTCCTAGCGTGGCGAAAAGATTTTAACCTAAGAGTTTT
GTGAATGTGCATGATTTTAAAAACCTTGATGAAGCGATTGATTACGTGAGATACTTGCACACGCACCCAAA
CGCTTATTTAGACATGCTCTATGAAAACCTTTAAACACCTTGATGGGAAAGCTTACTTTTACCAAGATT
TGAGTTTTAAAAAATCCTAGATTTTTTTAAACGATTTTAGAAAACGATACGATCTATCACAATAACCCT
TTTGTTTTCTATCGTGATTTGAATGAGCCGTTAGTATCTATTGATGATTTGAGAGCCGATTATAATAATTT
GAGAGCCGATTATAATAATTTGAGAGCCGATTATAATAATTTGAGAGCCGATTATAATAATTTGAGAGCCG
ATTACGATCGCTGTACAAAACCGTTCGCCTTTGTTGGAACCTCTCTCAAAACACCACTTTTAAATCTAT
CACAAAGCTTATCACAAATCCTTACCTTTGTTGCGTGCCATAAGGAGATGGGTAAAAAATTTGGGTTTGta
aAATTGGGGGTAAATCAAACCCCTTGCGCTATCATCGCAGACGCCACTTTTCTAAAACCAGCGATATTAGCC
CCTAAAACAAAATAGTAGGGTCTTTAAACTCTTTAGCGGTTTGAGAGACATTTTTATAAATCTCTTTCAT
GATGTGGTGTAATTTTCGCATCCACCACTTCAAACTCCAAGGGTGCATGCTCGCGTTTTGCGCCATTTCCA
AGCCGCTCACGCTCACCCCCCAGCATTAGCCGCCTTGCCCTATACCATAAGAAATCTTAGCCTGTAAAAAC
AATCAATCGCTTCATTGCTTGAGGGCATGTTTCGCCCTTCAGCCACGCATTTGCACCCATTAGAAAGGAG
GGTTTTGCGgaattc

Strain 802FutA fucosyltransferase amino acid sequence (SEQ ID NO:18)

MFQPLLDAFIESASIKKMPLSYPLKIAVANWWGGAEEFKKSAMYFILSQRYTITLHQNPNEPSDLVFGSP
IGAARKILSYQNTKRVPFYAGENEVNFNLFDYAIGFDELDLRDRYLRMPLYYDRLHHKAESVNDTTAPYKI
KPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKRGFASFVASNPAPKRNAFYDALNSIEPVTGGGSVK
TLGYKVGKNKNEFLSQYKFNLCFENSQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNF
DEAIDYVRYLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTI LENDTIYHNNPFVYRDLNE
PLVSIDDLRADYNNLRADYNNLRADYNNLRADYNNLRADYDRLLQNRSPLELSQNTTFKIYHKAYHKS
LLRAIRRWVKLGL

FIGURE 20

Strain 948FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:19)

ggatccCGGCGTGAATTACTACCTTTCTGGCTTGCACAGCTATGCCGCGAGGCGATCCCTTGCCCATCCCCA
CTTTCTTATACTTTTAAATAGCGATACCTTTTGCTCTCGTGATCTTGGCGTATTTCAAACGCCATTTGAGT
TTGCCTAAATTGGTTTAAAGGATAAAAAatggtccagcccttactagacgctttcatagacagcaccattt
agatgaaacaaccataagccccattaaatgtagccctagccaattggtggcccttaaaaaatagcgaaa
aaaaaggattcagagacttcattttgcatttcctctaaacaacgctataaaatcattctgcacagcaac
cctaatagaaccctcagatctagtctttggcaatcctttggaacaagccagaaaaatcttatcttatcaaaa
cactaaacgagtggttttacaccggcgaaaatgaagtgcctaatttcaatctctttgattacgccataggct
ttgatgaattggattttaacgatcgctatttgagaatgcctttgtattacgcctatttgcattataaagcc
atgcttggttaatgacaccacttcgcccataaaactcaaagccctttatactttaaaaaaaccttcccataa
atftaaagaaaaccaccccaatttatgtgcgctaatacacaacgagagcgatccttggaaaagagggttg
ccagttttgtcgcaagcaatcctaacgctcccacagaaacgctttctatgacgctttaaatgctattgag
ccagtggttagtgaggaggagtggtgaaaaaactctaggctataaggtcaaaaaacaaaacgaatttttaag
ccaatacaagttcaacctctggtttgaaaactcacaaggctatggctatgtaaccgaaaaaatccttgatg
cgtatttcagccacactatccctatttatgggggagtcacagcggtggcgaaagattttaaccctaaaagt
tttgatgaatgtgcatgatttcaacaactttgatgaagcgattgatttatatcagatatttacacgcgaccca
aaacgcttatttagacatgctttatgaaaaccctttaaacaccattgatgggaaagcgggtttttaccaag
atftgagttttgaaaagatcttagattttttcaaaaacattcttgaaaacgatacgatttatcattgcaat
gatgccattattctgctcttcacgctgatttgaaatgagccggttagtgctctggtgatgatttgagaagaga
tcatgatgatttgagggttaattatgatgatttgagagtttaattatgatgatttgagagtttaattatgatg
atftgagagtttaattatgatgatttgagagtttaattatgatgatttgagaagagatcatgatgatttgaga
agagatcatgaacgcctcttatcaaaaggctacccctttattggagctatcccaaaacacctcttttaaaat
ctatcgcaaagcttatcaaaagcttacccttggtgctgcccataaAAACAATTCAATCGCTTCATTGCT
TGAGGGCATGTTTCGCCCTTCAGCCACGCATTTGCACCCATTAGAAAGGAGGGTTTTGCGGAATTCCTGCA
GCCCGGGGGATCCCCGGGCTGCAGgaattc

Strain 948FutA fucosyltransferase amino acid sequence (SEQ ID NO:20)

MFQPLLDADFIDSTHLDETTHKPPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKIILHSNPNEPSDLVF
GNPLEQARKILSYQNTKRVFYTGNEVPNPNFLFDYAIGFDELDFNDRYLRMPLYYAYLHYKAMLVNDTTS
YKLKALYTLKKPSHKFKENHPNLCAIHNESDPWKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVK
NTLGYKVKNKNEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN
FDEAIDYIRYLHAHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFKNILENDTIYHCNDAHYSALHR
DLNEPLVSVDLRRDHDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRRDHDDLRRDHERLLSK
ATPLLELSQNTSFKIYRKAYQKSLPLLRAI

FIGURE 21

Strain 955FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:21)

ggatccCGAGCGACCAATCATTACAGGGATTTATTAAATTTAGATGTGGCTTTTCAGTAACACGCTGATAGT
GGAAAATGGTGCCTTAAACGGCTTGGTTACGGGGCATATGATGTTTTTCACACTCTAAAGGCGAAATGCTTC
TCGCCCTACAACGCTTGCTAAATATCAGTGAAACGAGCACTTTAGTTGTGGGCGATGGAGCGAATGACTTG
AGCatgTTCAAACATGCCCATATTAAATCGCTTTCACGCTAAAGAGGTTTTTAAACAACACGCCACGCA
TTGCATCAATGAGCCTGATTTAGCCCTAATCAAGCCTTTGATTTAAAAAATTTTTTTTGTAAAAATACTCCT
TTAAAGGATAAAGATGTTCCAGCCCCATTAGATGCCCTTCATAGAAAGCGCTTCAATTAAAAAAAATTTGC
CTCTAAATCTCCCCCCCCCTAAAAATCGCTGTGGCGAATTGGTTTAACGGCACTAAAGAATTTAAAGCGAG
CGTTCCTTTATTTTCATCCTAAACAACGCTATAAAATCATTCTGCACAGCAACCCTAATGAACCTCAGATC
TAGTCTTTGGCAATCCTTTGGAACAAGCCAGAAAAATCTTATCTTATCAAAACACTAAACGAGTGTTTTAC
ACCGGCGAAAATGAAGTGCCTAATTTCAATCTCTTTGATTACGCCATAGGCTTTGATGAATTGGATTTTAA
CGATCGCTATTTGAGAATGCCTTTGTATTACGCCTATTTGCATTATAAAGCCATGCTTGTAAATGACACCA
CTTCGCCCTATAAACTCAAAGCCCTTTATACTTTAAAAAACCTTCCCATAAATTTAAAGAAAACCACCCC
AATTTATGTGCGCTAATCCATAACGAGAGCGATCCTTGGAAAAGAGGGTTTGCCAGTTTTGTGCGAAGCAA
TCCTAACGCTCCCATCAGAAACGCTTCTATGACGCTTTAAATGCTATTGAGCCAGTGGCTAGTGGAGGGA
GTGTGAAAAACACTCTAGGCTATAAGGTCAAAAACAAAACGAATTTTAAAGCCAATACAAGTTCAACCTC
TGTTTTGAAAACTCACAAGGCTATGGCTATGTAACCGAAAAAATTCCTTGATGCGTATTTAGCCACACTA
TCCCTATTTATTGGGGGAGTCCCAGCGTGGCGAAAAGATTTTAAACCCTAAAAAGTTTTGTGAATGTGCATGAT
TTCAACAACCTTTGATGAAGCGATTGATTATATCAGATATTTACACGCGCACCAAAACGCTTATTTAGACAT
GCTTTATGAAAACCCCTTAAACACCATTGATGGGAAAGCGGGTTTTTACCAAGATTTGAGTTTTGAAAAGA
TCTTAGATTTTTTCAAAAACATTCTTGAAAACGATACGATTTATCATTGCAATGATGCCCATTTATTCTGCT
CTTCATCGTGATTTGAATGAGCCGTTAGTGTCTGTTGATGATTTGAGAAGAGATCATGATGATTTGAGGGT
TAATTATGATGATTTGAGAAGAGATCATGAACGCCTCTTATCAAAGGCTACCCCTCTTTTGGAGCTATCCC
AAAACACCTCTTTTAAATCTATCGCAAAGCTTATCAAAAGTCCTTACCCTTGTTGCGTGCCATAAGGAAG
TGGGTAAAAAATAAGGCGTATTTTAAAGACTGATGAAGAAATTGAAGCGCTATTTTAAATGCGCTAACGC
TTCTTTTTTGGAGCGTGGGGTTTTTGAGCATGTCCTCTAAAGCATGGGTGCTTAAAAATGTTTTGTTTTTA
AAGACACGATGCGTCCAAAGGATTCTTCTTTAGAAAGGTTTAAAGGCGTTTGGGCAAAATCTCGCCAAAT
ACCACAATGACTTTTGAAGCGCTGTTGTCTAATTGCCAGGTCGgaattc

Strain 955FutA fucosyltransferase amino acid sequence (SEQ ID NO:22)

MFKHAHIKIAFNAKEVLKQHATHCINEPDLALIKPLIFKIFFVKYSFKG . RCSSPY . MPS . KALQLKKNCL
 . ISPPLKIAVANWFNGTKEFKASVLYFILKQRYKII LHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYT
GENEVPNPNLFDYAIGFDELDFNDRYLRMPLYAYLHYKAMLVNDTTSPLYKLKALYTLKKPSHKFKENHPN
LCALIHNESDPWKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGKVKKNKNEFLSQQYKFNLC
FENSQGYGYVTEKIP . CVFQPHYPYLLGESQRGERR . P . KFCECA . FQQL . . SD . LYQIFTRAPKRLFRHA
L . KPLKHH . WESGFLPRFEF . KDLRFFQKHS . KRYDLSLQ . CPLFCSSS . FE . AVSVC . . FEKRS . . FEG .
L . . FEKRS . TPLIKGYPSFGAIPKHLF . NLSQSLSKVLTLVACHKEVG . KIRRI LRMLKMLKRYFKMR . RF
FFERGVFEHVL . SMGA . KMFCF . RHDASKGFFFRKV . KAFGQNLAKYHND . SAVV . LPGRN

FIGURE 22

Strain 1218FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:23)

ggatccTCTGGCTTGACAGCTATGCCGAGGCGATCCCTTGCCTATCCCTACTTTCTTATACCTTTTGG
TAGCGATACCTTTTCGCTCTCGTGATCTTGGCTTATTTCAAACGCCATTTGAGTTTGCCTAAATTGGTTTAA
AGGATAACCATGTTCCAACCCCTATTAGACGCTTATATAGAAAGCGCTTCCATTGAAAAAATTACCTCTAA
ATCTCCCCCCCCCTAAAAATCGCTGTGGCGAATTGGTGGGGAGATGAAGAGGTTGAAGAATTTAAAAAGA
ACATTCCTTTATTTTATTCTCAGTCAGCATTACACAATCACCCCTCCACCAAAACCCCAACGAACCCCTCCGAT
CTCGTCTTTGGCAGTCCTATTGGATCAGCCAGAAAAATCTTATCCTATCAAAACGCAAAAAGAGTGTTTTA
CACCGGTGAAAACGAATCGCCTAATTTCAACCTCTTTGATTACGCCATAGGCTTTGATGAATGGATTTTAG
AGATCGTTATTTAAGAATGCCTTTATATTATGATAGACTACACCATAAAGCCGAGAGCGTGAATGACACCA
CTTCGCCCTTACAACTCAAACCTGACAGCCTTTATGCTTTAAAAAAACCCTCCCATCATTTTAAAGAAAAAC
CACCCCAATTTATGCGCAGTAGTGAACAATGAGAGCGATCCTTTGAAAAGAGGGTTTGCAGATTTTGTAGC
GAGCAACCCTAACGCTCCTAAAAGGAATGCTTTCTATGACGCTTTAAATTCTATAGAGCCAGTTATTGGGG
GAGGGAGCGTGAAAACACTTTAGGCTATAACATTAAAAACAAGAGCGAGTTTTTAAAGCCAATACAAATTC
AATCTGTGTTTTGAAAACCTACAAGGCTATGGCTATGTAACCTGAAAAAATCATTGACGCTTACTTTAGCCA
TACCATTCTATTTATTGGGGGAGTCTAGCGTGGCACAAGATTTTAAACCCTAAGAGTTTTGTGAATGTTT
GTGATTTTAAAGATTTTGTATGAAGCGATTGATCATGTGCGATACTTGCACACGCACCCAAACGCTTATTTA
GACATGCTTTTATGAAAACCCCTTTAAACACCCTTGATGGGAAAAGCTTACTTTCCAAAATTTGAGTTTTAAAA
AAATCCTAGATTTTTTTTAAACGATCTTAGAAAACGACACGATTTATCACGATAACCCCTTTATTTTTTAT
CGTGATTTGAATGAGCCGTTAATATCTATTGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTA
TGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGATGATT
TGAGGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTT
AATTGTGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGAGCGGCTCTTACAAAACGCCTC
GCCTTTATTAGAACTCTCTCAAAACACCACTTTTAAAATCTATCGCAAAGCTTATCAAAAATCCTTACCTT
TGTTGCGTGCGGCGAGAAAGTTGATTAAAAAATTGGGTTTGTAATAATTGGGGGTAATCAAAACCCCTTGCGC
TATCATCGCAGACGCCACCTTTCTAAAACCAGCGATATTAGCCCTAAAACAAAATTAGTAGGGTCTTTAA
ACTCTTTAGCGGTTTGAGAGACATTCTTATAAgaattc

Strain 1218FutA fucosyltransferase amino acid sequence (SEQ ID NO:24)

MFQPLLDAYIESASIEKITSKSPPLKIAVANWWGDEEVEEFKKNILYFILSQHYTITLHQNPNEPSDLVF
GSPIGSARKILSYQNAKRIFYTGENESPNFNLFDAIGFDEWILEIVI . ECLYIMIDYTIKPR . MTPRLR
TNSNLTAFML . KNPPILKKTPIYAQ . . TMRAIL . KEGLRVL . RATLTLLKGMLSMTL . IL . SOLLGEA
 . KTL . AITLKTRASF . ANTNSICVLKTHKAMAM . LKKSLLTLAIPFLFIGGVLAWHKILTLRVL . MFVIL
KILMKRLIMCDTCTRTQTLI . TCFMCTL . TPLMGKLTQNLSEFKKILDFFKTILENDTIYHDNPFIFYRDL
NEPLISIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV
DLRVNYDDLRVNYERLLQNASPLLELSQNTTFKIYRKAYQKSLPLLRAARKLIKLG . NWG . SNPLRYHR
RRHLSKTSDISP . NKISRVFKLFSGLRDILIRYQAYRYRRPRGGAR